

# SEQUENCE LISTING

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<120> A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBM4,  
EXPRESSED HIGHLY IN PROSTATE, COLON, AND LUNG

<130> D0039NP/3053-4117US3

<140> TBA

<141> 2001-09-26

<150> 60/235,833

<151> 2000-09-27

<150> 60/261,776

<151> 2001-01-16

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<151> 2001-07-13

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<151> 2001-08-17

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<170> PatentIn Ver. 2.1

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gctgtgctag gtaacttgac aatcatctac attgtgcgga ctgagcacag cctgcatgag 180  
cccctgtata tatttctttg catgctttca ggcattgaca tcctcatctc caccctatcc 240  
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ctgctacaga tgtttgccat ccactcctta tctggcatgg aatccacagt gctgctggcc 360  
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cccttctctg tcttcatcaa gcagctgccc ttctgccgct ccaatatcct ttccattcc 540  
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Pro Leu Cys Ser Leu Tyr Leu Ile Ala Val Leu Gly Asn Leu Thr Ile  
 35 40 45

Ile Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met Tyr Ile  
 50 55 60

Phe Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr Ser Ser  
 65 70 75 80

Met Pro Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln  
 85 90 95

Phe Asp Ala Cys Leu Leu Gln Met Phe Ala Ile His Ser Leu Ser Gly  
 100 105 110

Met Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala  
 115 120 125

Ile Cys His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro Arg Val  
 130 135 140

Thr Lys Ile Gly Val Ala Ala Val Val Arg Gly Ala Ala Leu Met Ala  
 145 150 155 160

Pro Leu Pro Val Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile  
 165 170 175

**Figure 1**

**Figure 1**

**Figure 6**

[illegible][illegible]

**Figure 1**

**Figure 1**

**Figure 1**

**Figure 1**

**Figure 6.**

**Figure 1**

**Figure 1**

**Figure 1**

[illegible]

**Figure 1**

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 aagcagacga aaggaacagt aataggaaga tctagcaagg atgtggtggg gcagtttcag 960  
 tgtgagatgc catggacagg aaaatggcag catatgtgtg tgtgtgtgtg tgtgtgtgtg 1020  
 tccatgagac agagagacat aaataactaa ataaaaaggc atatcacaaa gaggggctcc 1080  
 tgcttcagct tgagtcctgg atgcaaagac atgtggactg ggaactcagc aacctatctg 1140  
 cagccaagga catgacgtta gacgcccacaa gaaaaggaaa attggtcaca cataggaaga 1200  
 gcactcaagt gccagctaca gtgaatgaca aataccacac acaagcaca gctctacatt 1260  
 cacaaaaact tggaaaacac aagttcatag actgggcaac cctgagtagt ggagagatca 1320  
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 tttttacatg cagtccaact cttaactgct tctactgatg tcttaacaga tcttgagata 300  
 agaatggtac atctagagaa catttgccaa aggcctaagc acggcaaaagg aaaataaaca 360  
 cagaataataa taaaatgaga taactctagc taaaactata acttctctct cagaactccc 420  
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 cctgtttttc ctatttaatt ttcttatcaa ccttttaatt aggcacaagt attattagta 660  
 ccctcattgt agccatggga aaattgatgt tcagtgggga tcagtgaatt aaatggggtc 720  
 atacaagtat aaaaattaaa aaaaaaagac ttcatgccca atctcatatg atgtggaaga 780  
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 cctgtgtctt ggaagaagtg attttcaggt tcaccattat ggaagattct tattcgaaaa 1020  
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 gctttatttg gggctttgtg cagtatggaa cagggaactt gagaccaga aagcaatctg 1260  
 acttaggcac ggggaatcagg catttttgc tctgaggggc tattaccaag gtttaaatgg 1320  
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 aatgtcatct ctgttcatca ttgactgctc ttgtctcatc attgaatccc ccagcaaaagt 1620  
 gcctagaaca taatagtgtc tatgcttgac accggttatt ttcatcaaaa cctgattcct 1680  
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20 25 30

Tyr Phe Ser Ile Ile Val Gly Asn Gly Thr Leu Leu Phe Ile Ile Trp  
35 40 45

Ser Asp His Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Ala Val Leu  
50 55 60

Ala Ser Met Asp Leu Gly Met Thr Leu Thr Thr Met Pro Thr Val Leu  
65 70 75 80

Gly Val Leu Val Leu Asn Gln Arg Glu Ile Val His Gly Ala Cys Phe  
85 90 95

Ile Gln Ser Tyr Phe Ile His Ser Leu Ala Ile Val Glu Ser Gly Val  
100 105 110

Leu Leu Ala Met Ser Tyr Asp Arg Phe Val Ala Ile Cys Thr Pro Leu  
115 120 125

His Tyr Asn Ser Ile Leu Thr Asn Ser Arg Val Met Lys Met Ala Leu  
130 135 140

Gly Ala Leu Leu Arg Gly Phe Val Ser Ile Val Pro Pro Ile Met Pro  
145                      150                      155                      160

Leu Phe Trp Phe Pro Tyr Cys His Ser His Val Leu Ser His Ala Phe  
165 170 175

Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Ala Asp Ile Thr Phe  
180 185 190

Asn Leu Ile Tyr Pro Val Val Leu Val Ala Leu Thr Phe Phe Leu Asp  
195 200 205

Ala Leu Ile Ile Ile Phe Ser Tyr Val Leu Ile Leu Lys Lys Val Met  
210 215 220

Gly Ile Ala Ser Gly Glu Glu Arg Lys Lys Ser Leu Asn Thr Cys Val

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 Ser His Ile Ser Cys Val Leu Val Phe Tyr Ile Thr Val Ile Gly Leu  
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 Thr Phe Ile His Arg Phe Gly Lys Asn Ala Pro His Val Val His Ile  
                          260                      265                      270  
 Thr Met Ser Tyr Val Tyr Phe Leu Phe Pro Pro Phe Met Asn Pro Ile  
                          275                      280                      285  
 Ile Tyr Ser Ile Lys Thr Lys Gln Ile Gln Arg Ser Ile Leu Arg Leu  
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 Leu Ser Lys His Ser Arg Thr  
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 Tyr Ile Ser Val Leu Leu Gly Asn Gly Thr Leu Leu Tyr Leu Ile Lys  
                          35                                      40                                      45  
 Asp Asp His Asn Leu His Glu Pro Met Tyr Tyr Phe Leu Ala Met Leu  
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 Ala Gly Thr Asp Leu Thr Val Thr Leu Thr Thr Met Pro Thr Val Met  
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 Ala Val Leu Trp Val Asn His Arg Glu Ile Arg His Gly Ala Cys Phe  
                          85                                      90                                      95  
 Leu Gln Ala Tyr Ile Ile His Ser Leu Ser Ile Val Glu Ser Gly Val  
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Gly Val Val Leu Arg Gly Phe Leu Ser Leu Val Pro Pro Ile Leu Pro  
145 150 155 160

Leu Phe Trp Phe Ser Tyr Cys Arg Ser His Val Leu Ser His Ala Phe  
165 170 175

Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Ala Asp Ile Thr Phe  
180 185 190

Asn Arg Ile Tyr Pro Val Val Leu Val Ala Leu Thr Phe Phe Leu Asp  
195 200 205

Ala Leu Ile Ile Val Phe Ser Tyr Val Leu Ile Leu Lys Thr Val Met  
210 215 220

Gly Ile Ala Ser Gly Glu Glu Arg Ala Lys Ala Leu Asn Thr Cys Val  
225 230 235 240

Ser His Ile Ser Cys Val Leu Val Phe Tyr Ile Thr Val Ile Gly Leu  
245 250 255

Thr Phe Ile His Arg Phe Gly Lys Asn Ala Pro His Val Val His Ile  
260 265 270

Thr Met Ser Tyr Val Tyr Phe Leu Phe Pro Pro Phe Met Asn Pro Ile  
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Leu Ser Val  
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Tyr Val Cys Ile Leu Leu Gly Asn Gly Met Leu Leu Tyr Leu Ile Lys  
35 40 45

His Asp His Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Thr Met Leu  
50 55 60

Ala Gly Thr Asp Leu Met Val Thr Leu Thr Thr Met Pro Thr Val Met  
65 70 75 80

Gly Ile Leu Trp Val Asn His Arg Glu Ile Ser Ser Val Gly Cys Phe  
85 90 95

Leu Gln Ala Tyr Phe Ile His Ser Leu Ser Val Val Glu Ser Gly Ser  
100 105 110

Leu Leu Ala Met Ala Tyr Asp Arg Phe Ile Ala Ile Arg Asn Pro Leu  
115 120 125

Arg Tyr Ala Ser Ile Phe Thr Asn Thr Arg Val Ile Ala Leu Gly Val  
130 135 140

Gly Val Phe Leu Arg Gly Phe Val Ser Ile Leu Pro Val Ile Leu Arg  
145 150 155 160

Leu Phe Ser Phe Ser Tyr Cys Lys Ser His Val Ile Thr Arg Ala Phe  
165 170 175

Cys Leu His Gln Glu Ile Met Arg Leu Ala Cys Ala Asp Ile Thr Phe  
180 185 190

Asn Arg Leu Tyr Pro Val Ile Leu Ile Ser Leu Thr Ile Phe Leu Asp  
195 200 205

Ser Leu Ile Ile Leu Phe Ser Tyr Ile Leu Ile Leu Asn Thr Val Ile  
210 215 220

Gly Ile Ala Ser Gly Glu Glu Gln Thr Lys Ala Leu Asn Thr Cys Val  
225 230 235 240

Ser His Phe Cys Ala Val Leu Ile Phe Tyr Ile Pro Leu Ala Gly Leu  
245 250 255

Ser Ile Ile His Arg Tyr Gly Arg Asn Ala Pro Pro Ile Ser His Ala  
260 265 270

Val Met Ala Asn Val Tyr Leu Phe Val Pro Pro Ile Leu Asn Pro Val  
275 280 285



180

185

190

Thr Leu Asn Ser Leu Tyr Gly Leu Ile Leu Val Leu Val Ala Ile Leu  
195 200 205

Asp Phe Val Leu Ile Ala Leu Ser Tyr Ile Met Ile Phe Arg Thr Val  
210 215 220

Leu Gly Ile Thr Ser Lys Glu Glu Gln Thr Lys Ala Leu Asn Thr Cys  
225                      230                      235                      240

Val Ser His Phe Cys Ala Val Leu Ile Phe Tyr Ile Pro Leu Ala Gly  
245 250 255

Leu Ser Ile Ile His Arg Tyr Gly Arg Asn Ala Pro Pro Ile Ser His  
260 265 270

Ala Val Met Ala Asn Val Tyr Leu Phe Val Pro Pro Ile Leu Asn Pro  
275 280 285

Val Leu Tyr Ser Met Lys Ser Lys Ala Ile Cys Lys Gly Leu Leu Arg  
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Met Tyr Ala Val Ala Leu Phe Gly Asn Cys Ile Val Val Phe Ile Val  
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Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met  
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Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile  
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 <213> MOUSE

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Thr Trp Leu Ser Ile Pro Phe Cys Leu Met Tyr Ile Ala Ala Val Leu  
 35 40 45

Gly Asn Gly Ala Leu Ile Leu Val Val Leu Ser Glu Arg Thr Leu His  
 50 55 60

Glu Pro Met Tyr Val Phe Leu Ser Met Leu Ala Gly Thr Asp Ile Leu  
 65 70 75 80

Leu Ser Thr Thr Thr Val Pro Lys Thr Leu Ala Ile Phe Trp Phe His  
 85 90 95

Ala Gly Glu Ile Pro Phe Asp Ala Cys Ile Ala Gln Met Phe Phe Ile  
 100 105 110

His Val Ala Phe Val Ala Glu Ser Gly Ile Leu Leu Ala Met Ala Phe  
 115 120 125

Asp Arg Tyr Val Ala Ile Cys Thr Pro Leu Arg Tyr Ser Ala Val Leu  
 130 135 140

Thr Pro Met Ala Ile Gly Lys Met Thr Leu Ala Ile Trp Gly Arg Ser  
 145 150 155 160

Ile Gly Thr Ile Phe Pro Ile Ile Phe Leu Leu Lys Arg Leu Ser Tyr  
 165 170 175

Cys Arg Thr Asn Val Ile Pro His Ser Tyr Cys Glu His Ile Gly Val  
 180 185 190

Ala Arg Leu Ala Cys Ala Asp Ile Thr Val Asn Ile Trp Tyr Gly Phe  
 195 200 205

Ser Val Pro Met Ala Ser Val Leu Val Asp Val Ala Leu Ile Gly Ile  
 210 215 220

Ser Tyr Thr Leu Ile Leu Gln Ala Val Phe Arg Leu Pro Ser Gln Asp  
225 230 235 240

Ala Arg His Lys Ala Leu Asn Thr Cys Gly Ser His Ile Gly Val Ile  
245 250 255

Leu Leu Phe Phe Ile Pro Ser Phe Phe Thr Phe Leu Thr His Arg Phe  
260 265 270

Gly Lys Asn Ile Pro His His Val His Ile Leu Leu Ala Asn Leu Tyr  
275 280 285

Val Leu Val Pro Pro Met Leu Asn Pro Ile Ile Tyr Gly Ala Lys Thr  
290 295 300

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305 310 315 320

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Ile Ala Ile Pro Ile Cys Ser Met Tyr Ile Val Ala Val Ile Gly Asn  
35 40 45

Val Leu Leu Ile Phe Leu Ile Val Thr Glu Arg Ser Leu His Glu Pro  
50 55 60

Met Tyr Phe Phe Leu Ser Met Leu Ala Leu Ala Asp Leu Leu Leu Ser  
65 70 75 80

Thr Ala Thr Ala Pro Lys Met Leu Ala Ile Phe Trp Phe His Ser Arg  
85 90 95

Gly Ile Ser Phe Gly Ser Cys Val Ser Gln Met Phe Phe Ile His Phe

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Ile Phe Val Ala Glu Ser Ala	Ile Leu Leu Ala Met Ala	Phe Asp Arg
115	120	125
Tyr Val Ala Ile Cys Tyr Pro	Leu Arg Tyr Thr Thr	Ile Leu Thr Ser
130	135	140
Ser Val Ile Gly Lys Ile Gly Thr	Ala Ala Val Val Arg Ser	Phe Leu
145	150	155
Ile Cys Phe Pro Phe Ile Phe	Leu Val Tyr Arg Leu Leu Tyr	Cys Gly
165	170	175
Lys His Ile Ile Pro His Ser Tyr	Cys Glu His Met Gly Ile Ala Arg	
180	185	190
Leu Ala Cys Asp Asn Ile Thr Val	Asn Ile Ile Tyr Gly Leu Thr Met	
195	200	205
Ala Leu Leu Ser Thr Gly Leu Asp	Ile Leu Leu Ile Ile Ile Ser Tyr	
210	215	220
Thr Met Ile Leu Arg Thr Val Phe	Gln Ile Pro Ser Trp Ala Ala Arg	
225	230	235
Tyr Lys Ala Leu Asn Thr Cys Gly	Ser His Ile Cys Val Ile Leu Leu	
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Phe Tyr Thr Pro Ala Phe Phe Ser	Phe Phe Ala His Arg Phe Gly Gly	
260	265	270
Lys Thr Val Pro Arg His Ile His	Ile Leu Val Ala Asn Leu Tyr Val	
275	280	285
Val Val Pro Pro Met Leu Asn Pro	Ile Ile Tyr Gly Val Lys Thr Lys	
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Gln His Asp Ser Arg Cys		
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Phe Gly Thr Val Tyr Leu Ile Ala Val Leu Gly Asn Val Ile Ile Leu  
35 40 45

Phe Val Ile Tyr Leu Glu His Ser Leu His Gln Pro Met Phe Tyr Leu  
50 55 60

Leu Ala Ile Leu Ala Val Thr Asp Leu Gly Leu Ser Thr Ala Thr Val  
65 70 75 80

Pro Arg Ala Leu Gly Ile Phe Trp Phe Gly Phe His Lys Ile Ala Phe  
85 90 95

Arg Asp Cys Val Ala Gln Met Phe Phe Ile His Leu Phe Thr Gly Ile  
100 105 110

Glu Thr Phe Met Leu Val Ala Met Ala Phe Asp Arg Tyr Ile Ala Ile  
115 120 125

Cys Asn Pro Leu Arg Tyr Asn Thr Ile Leu Thr Asn Arg Thr Ile Cys  
130 135 140

Ile Ile Val Gly Val Gly Leu Phe Lys Asn Phe Ile Leu Val Phe Pro  
145                    150                    155                    160

Leu Ile Phe Leu Ile Leu Arg Leu Ser Phe Cys Gly His Asn Ile Ile  
165 170 175

Pro His Thr Tyr Cys Glu His Met Gly Ile Ala Arg Leu Ala Cys Val  
180 185 190

Ser Ile Lys Val Asn Val Leu Phe Gly Leu Ile Leu Ile Ser Met Ile  
195 200 205

Leu Leu Asp Val Val Leu Ser Ala Leu Ser Tyr Ala Lys Ile Leu His  
210 215 220

Ala Val Phe Lys Leu Pro Ser Trp Glu Ala Arg Leu Lys Ala Leu Asn  
225                      230                      235                      240



Thr Cys Gly Ser His Val Cys Val Ile Leu Ala Phe Phe Thr Pro Ala  
245 250 255

Phe Phe Ser Phe Leu Thr His Arg Phe Gly His Asn Ile Pro Arg Tyr  
260 265 270

Ile His Ile Leu Leu Ala Asn Leu Tyr Val Ile Ile Pro Xaa Ala Leu  
275 280 285

Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys Gln Ile Gln Asp Arg Ala  
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Val Thr Ile Leu Cys Asn Glu Val Gly Gln Leu Ala Asp Asp  
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Phe Cys Val Met Tyr Ile Ile Ala Met Ile Gly Asn Ser Leu Ile Leu  
35 40 45

Val Ile Ile Lys Ser Glu Lys Ser Leu His Ile Pro Met Tyr Ile Phe  
50 55 60

Leu Ala Ile Leu Ala Val Thr Asp Ile Ala Leu Ser Thr Cys Ile Leu  
65 70 75 80

Pro Lys Met Leu Gly Ile Phe Trp Phe His Met Pro Gln Ile Ser Phe  
85 90 95

Asp Ala Cys Leu Leu Gln Met Glu Leu Ile His Ser Phe Gln Ala Thr  
100 105 110

Glu Ser Gly Ile Leu Leu Ala Met Ala Leu Asp Arg Tyr Val Ala Ile  
115 120 125

Cys Asn Pro Leu Arg His Ala Thr Ile Phe Ser Pro Gln Leu Thr Thr  
130 135 140

Cys Leu Gly Ala Gly Ala Leu Leu Arg Ser Leu Ile Thr Thr Phe Pro  
145 150 155 160

Leu Ile Leu Leu Ile Lys Phe Cys Leu Lys Tyr Phe Arg Thr Thr Ile  
165 170 175

Ile Ser His Ser Tyr Cys Glu His Met Ala Ile Val Lys Leu Ala Ala  
180 185 190

Gln Asp Ile Arg Ile Asn Lys Ile Cys Gly Leu Leu Val Ala Phe Ala  
195 200 205

Ile Leu Gly Phe Asp Ile Val Phe Ile Thr Phe Ser Tyr Val Arg Ile  
210 215 220

Phe Ile Thr Val Phe Gln Leu Pro Gln Lys Glu Ala Arg Phe Lys Ala  
225 230 235 240

Phe Asn Thr Cys Ile Ala His Ile Cys Val Phe Leu Gln Phe Tyr Leu  
245 250 255

Leu Ala Phe Phe Ser Phe Phe Thr His Arg Phe Gly Ala His Ile Pro  
260 265 270

Pro Tyr Val His Ile Leu Leu Ser Asp Leu Tyr Leu Leu Val Pro Pro  
275 280 285

Phe Leu Asn Pro Ile Val Tyr Gly Ile Lys Thr Lys Gln Ile Arg Asp  
290 295 300

Gln Val Leu Lys Met Phe Phe Ser Lys Lys Pro Leu  
305 310 315

<210> 17

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized  
peptide

<400> 17

Met Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile  
1 5 10 15

Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln  
20 25

<210> 18  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthesized  
peptide

<400> 18  
Arg Thr Glu His Ser Leu His Glu Pro Met Tyr  
1 5 10

<210> 19  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthesized  
peptide

<400> 19  
Asn Ser Thr Thr Ile Gln Phe Asp Ala Cys Leu Leu Gln Met  
1 5 10

<210> 20  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthesized  
peptide

<400> 20  
His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro Arg Val Thr Lys  
1 5 10 15

<210> 21  
<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized  
peptide

<400> 21

Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile Leu Ser His Ser Tyr Cys  
1 5 10 15

Leu His Gln Asp Val Met Lys Leu Ala Cys Asp Asp Ile Arg  
20 25 30

<210> 22

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized  
peptide

<400> 22

Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys Ala  
1 5 10

<210> 23

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized  
peptide

<400> 23

His Arg Phe Ser Lys Arg Arg Asp Ser Pro  
1 5 10

<210> 24

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized  
peptide

<400> 24

Lys Thr Lys Glu Ile Arg Gln Arg Ile Leu Arg Leu Phe His Val Ala  
1 5 10 15

Thr His Ala Ser Glu Pro  
20

<210> 25

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Forward GPCR9  
primer-

<400> 25

cctgtgctca acccaattgt ct 22

<210> 26

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Reverse GPCR9  
primer-

<400> 26

actgacacct agggctctga ag 22

<210> 27

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GAPDH-F3  
forward primer

<400> 27

agccgagcca catcgct

17

<210> 28

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GAPDH-R1  
reverse primer

<400> 28

gtgaccaggc gcccaatac

19

<210> 29

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GAPDH-PVIC  
Taqman (R) Probe

<400> 29

caaatccgtt gactccgacc ttcacctt

28

<210> 30

<211> 39

<212> DNA

<213> Artificial Sequence

<400> 30

cccaagcttg caccatgatg gtggatccca atggcattg

39

<210> 31

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: HGPRBMY4 3'  
primer

<400> 31

gaagatctct agggctctga agcgtgtgtg gcc

33

<210> 32

<211> 59

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: HGPRBMY4 3'  
primer- Flag tag

<400> 32

gaagatctct acttgctgc gtcgtccttg tagtcacatgg gctctgaagc gtgtgtggc 59

<210> 33

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
polypeptide

<400> 33

Met Val His Arg Phe Ser Lys Arg Arg Asp Ser Pro Leu  
1 5 10

<210> 34

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
polypeptide

<400> 34

Val Arg Thr Glu His Ser Leu His Glu Pro Met Tyr Ile Phe  
1 5 10

<210> 35

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
polypeptide

<400> 35

Phe Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr  
1 5 10

<210> 36

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
polypeptide

<400> 36

Ala Ile His Ser Leu Ser Gly Met Glu Ser Thr Val Leu Leu  
1 5 10

<210> 37

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
polypeptide

<400> 37

His Arg Phe Ser Lys Arg Arg Asp Ser Pro Leu Pro Val Ile  
1 5 10

<210> 38

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
polypeptide

<400> 38



Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile  
1 5 10

<210> 39

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
polypeptide

<400> 39

Ile Ala Val Leu Gly Asn Leu Thr Ile Ile Tyr Ile Val Arg  
1 5 10

<210> 40

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
polypeptide

<400> 40

Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln Phe Asp Ala  
1 5 10

<210> 41

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
polypeptide

<400> 41

Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile Leu  
1 5 10 15

<210> 42

<211> 16

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<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 42
Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe Trp Leu Ala Phe
  1             5             10            15

<210> 43
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 43
Ile His Ser Leu Ser Gly Met Glu Ser Thr Val Leu Leu Ala Met Ala
  1             5             10            15

<210> 44
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 44
Gln Ala Lys Ala Phe Gly Thr Cys Val Ser His Val Cys Ala Val Phe
  1             5             10            15

<210> 45
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

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<400> 45

His Ser Leu Ser Gly Met Glu Ser Thr Val Leu Leu Ala Met Ala Phe  
1 5 10 15

Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg  
20 25

<210> 46

<211> 99

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo 1;  
N=A+G+C+T; K=C+G+T

<400> 46

cgaagcgtaa gggeccagcc ggccnnknkn nnknknknkn knknknknkn 60  
nnknknknkn nnknknknkn knkccgggt ccggcgggc 99

<210> 47

<211> 95

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo 2;  
N=A+G+C+T; V=C+A+G

<400> 47

aaaagggaaa aagcgccgc vnnvnnvnnv nnvnnvnnv nnvnnvnnv vnnvnnvnnv 60  
nnvnnvnnv nnvnnvnnv gccgcccga cccgg 95

<210> 48

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
polypeptide

<400> 48

Pro Gly Pro Gly Gly

1

5

&lt;210&gt; 49

&lt;211&gt; 38

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic 5'  
Primer

&lt;400&gt; 49

gcagcagcgg ccgccagttc tggttgcct tccattg

38

&lt;210&gt; 50

&lt;211&gt; 36

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic 3'  
Primer

&lt;400&gt; 50

gcagcagtcg acgggctctg aagcgtgtgt ggccac

36

&lt;210&gt; 51

&lt;211&gt; 39

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic 5'  
Primer

&lt;400&gt; 51

gcagcagcgg ccgcatgatg gtggatccca atggcaatg

39

&lt;210&gt; 52

&lt;211&gt; 37

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic 3'  
Primer

<400> 52  
gcagcagtcg accttcactc catagacaat tgggttg

37

<210> 53  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
polypeptide

<400> 53  
Gly Asp Phe Trp Tyr Glu Ala Cys Glu Ser Ser Cys Ala Phe Trp  
1 5 10 15

<210> 54  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
polypeptide

<400> 54  
Cys Leu Arg Ser Gly Thr Gly Cys Ala Phe Gln Leu Tyr Arg Phe  
1 5 10 15

<210> 55  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
polypeptide

<400> 55  
Phe Ala Gly Gln Ile Ile Trp Tyr Asp Ala Leu Asp Thr Leu Met  
1 5 10 15

<210> 56  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
       polypeptide

<400> 56  
 Leu Ile Phe Phe Asp Ala Arg Asp Cys Cys Phe Asn Glu Gln Leu  
       1                  5                  10                  15

<210> 57  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
       polypeptide

<400> 57  
 Leu Glu Trp Gly Ser Asp Val Phe Tyr Asp Val Tyr Asp Cys Cys  
       1                  5                  10                  15

<210> 58  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
       polypeptide

<400> 58  
 Arg Ile Val Pro Asn Gly Tyr Phe Asn Val His Gly Arg Ser Leu  
       1                  5                  10                  15

<210> 59  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
polypeptide

<400> 59

Trp Glu Arg Ser Ser Ala Gly Cys Ala Asp Gln Gln Tyr Arg Cys  
1 5 10 15

<210> 60

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
polypeptide

<400> 60

Tyr Phe Ser Asp Gly Glu Ser Phe Phe Glu Pro Gly Asp Cys Cys  
1 5 10 15